

A/red-neckedstint/WesternAus/4094/84	CY035897	CY035896	CY035895	CY035890	CY035893	CY035892	CY035891	CY035894
A/red-neckedstint/WesternAus/4126/80	CY033160	CY033159	CY033158	CY033153	CY033156	CY033155	CY033154	CY033157
A/red-neckedstint/WesternAus/4915/84	CY029904	CY029903	CY029902	CY029897	CY029900	CY029899	CY029898	CY029901
A/red-neckedstint/WesternAus/4923/83	CY028290	CY028289	CY028288	CY028283	CY028286	CY028285	CY028284	CY028287
A/red-neckedstint/WesternAus/5745/82	CY029880	CY029879	CY029878	CY029873	CY029876	CY029875	CY029874	CY029877
A/ruddyshelduck/Mongolia/37/05	GQ907341	GQ907340	GQ907339	GQ907334	GQ907337	GQ907336	GQ907335	GQ907338
A/ruddyshelduck/Mongolia/P52/05	GQ907349	GQ907348	GQ907347	GQ907342	GQ907345	GQ907344	GQ907343	GQ907346
A/sharp-tailedsandpiper/Aus/10/04	CY029888	CY029887	CY029886	CY029881	CY029884	CY029883	CY029882	CY029885
A/sharp-tailedsandpiper/Aus/6/04	CY025204	CY025203	CY025202	CY025197	CY025200	CY025199	CY025198	CY025201
A/shearwater/Aus/1/1973	CY005827	CY005826	CY005825	CY014656	CY014658	CY014657	CY005823	CY005824
A/shearwater/Aus/405/78	CY005665	CY005664	CY005663	CY014621	CY005661	CY014622	CY005660	CY005662
A/shearwater/Aus/751/75	CY045262	CY045261	CY045260	CY045255	CY045258	CY045257	CY045256	CY045259
A/shoveler/NL/19/99	CY005858	CY005857	CY005856	CY014719	CY005854	CY005853	CY005852	CY005855
A/slaty-backedgull/Japan/6KS0185/06	CY079298	CY079297	CY079296	CY079291	CY079294	CY079293	CY079292	CY079295
A/spotbillduck/Xuvi/6/05	GQ203122	GQ203123	GQ203124	GQ184327	GQ169500	GQ184332	GQ219713	GQ219714
A/swan/Slovenia/53/09	HQ283354	HQ283355	HQ283356	HQ283357	HQ283358	HQ283359	HQ283360	HQ283361
A/teal/Germany/WV632/05	CY061882	CY061883	CY061884	CY061885	CY061886	CY061887	CY061888	CY061889
A/teal/Italy/3812/05	CY022652	CY022651	CY022650	CY022645	CY022648	CY022647	CY022646	CY022649
A/teal/Italy/3931-38/05	CY022644	CY022643	CY022642	CY022637	CY022640	CY022639	CY022638	CY022641
A/tern/Aus/752/75	CY077659	CY077658	CY077657	CY077654	CY077655	CY077654	CY077653	CY077656
A/tuftedduck/PT/13771/06	HM849010	HM849009	HM849008	HM849003	HM849006	HM849005	HM849004	HM849007
A/turnstone/NL/1/07	CY041353	CY041352	CY041351	CY041346	CY041349	CY041348	CY041347	CY041350
A/wedge-tailedshearwater/WesternAus/405/77	CY028659	CY028658	CY028657	CY028652	CY028655	CY028654	CY028653	CY028656
A/whistlingswan/Shimane/468/88	GQ176105	GQ176106	GQ176107	GQ176112	GQ176109	GQ176110	GQ176111	GQ176108
A/whitefrontedgoose/NL/1/99	CY060428	CY060429	CY060430	CY060431	CY060432	CY060433	CY060434	CY060435
A/whitefrontedgoose/NL/2/99	CY060436	CY060437	CY060438	CY060439	CY060440	CY060441	CY060442	CY060443
A/whooperswan/Mongolia/232/05	GQ907357	GQ907356	GQ907355	GQ907350	GQ907353	GQ907352	GQ907351	GQ907354

*Sequences submitted to Genbank are depicted in bold

#Submitted as draft sequence, due to low coverage, low quality, ambiguities, frameshifts, gaps, or other problems.

Table S2. Statistically supported migration rates between regions for the whole-genome dataset.

	PB2	PB1	PA	HA	NP	NA	M	NS
East to West	0.64 [†] (0.01:1.62)		2.61 (0.29:5.35)	1.58 (0.10:3.47)			1.43 (0.03:3.24)	2.05 (0.44:4.16)
East to Central	0.93 (0.07:2.11)	0.87 (0.05:1.99)	0.76 (0.04:1.74)	0.65 (0.00:1.55)	1.48 (0.16:3.08)			0.71 (0.02:1.71)
East to Oceania	2.55 (0.67:4.81)	1.86 (0.40:3.67)	1.45 (0.24:3.01)	1.59 (0.19:3.27)	1.37 (0.16:3.08)	0.89 (0.00:1.97)	1.15 (0.04:2.56)	
West to Central	1.4 (0.25:2.81)	1.16 (0.13:2.40)	1.23 (0.18:2.54)	0.866 (0.12:1.84)	1 (0.01:2.21)	0.97 (0.78:1.98)	1.42 (0.16:2.91)	1.6 (0.37:3.11)
West to East	1.58 (0.35:3.12)	2.12 (0.39:4.27)		2.05 (0.47:3.96)	2.13 (0.11:4.27)	2.52 (0.56:4.69)	1.85 (0.24:3.83)	1.88 (0.39:3.70)
West to Oceania						0.73 (0.00:1.66)		0.87 (0.02:1.90)
Central to West								
Central to East				0.81 (0.00:1.99)			1.06 (0.00:2.66)	
Central to Oceania								
Oceania to West				1.16 (0.02:2.35)		0.95 (0.16:1.95)		
Oceania to Central								
Oceania to East					0.6 (0.00:1.52)		0.92 (0.00:2.19)	

* Only migration rates with a BF higher than 8 are shown

[†] Migration rates with a BF higher than 100 are depicted in bold

Legends

Figure S1. Maximum likelihood trees of (a) PB2 and PB2, (b) PA and HA, (c) NP and NA and (d) MP and NS, displaying the genetic diversity of avian influenza A viruses in Eurasian wild birds. The taxa color indicates the bird species group from which the sample was isolated: Dabbling ducks – blue, diving and other ducks – pink, geese – orange, swans – green, fowl – black, gulls and other shorebirds – red.

Figure S2. Maximum likelihood trees of (a) PB2 and PB2, (b) PA and HA, (c) NP and NA and (d) MP and NS, displaying the genetic diversity in different locations in Eurasia. The taxa color indicates the regional location from where the sample was isolated: Oceania - cyan, East Eurasia - red, Central Eurasia - green, West Eurasia – blue.

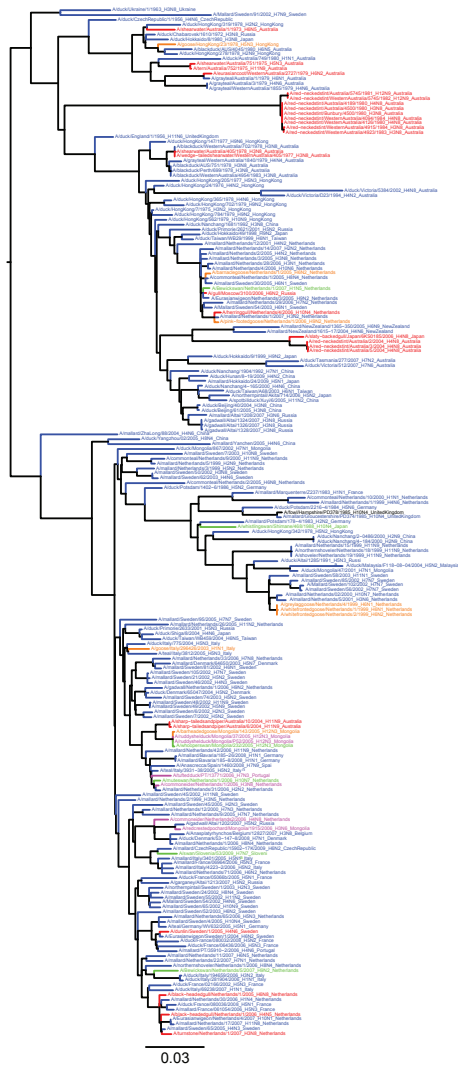
Figure S3.

Maximum clade credibility (MCC) trees, summarizing the results of the Bayesian phylogenetic inference of (a) PB2 and PB2, (b) PA and HA, (c) NP and NA and (d) MP and NS, displaying the genetic diversity in different locations in Eurasia. The taxa color indicates the regional location from where the sample was isolated: Oceania - cyan, Central Eurasia - green, East Eurasia - red, West Eurasia - blue.

The scale bar represents time in years

Figure S1a

PB2



PB1

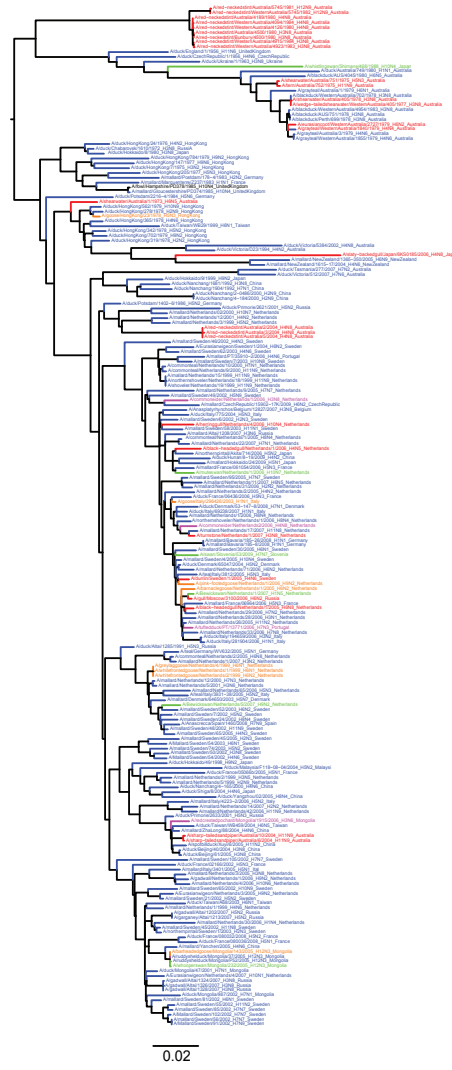


Figure S1b

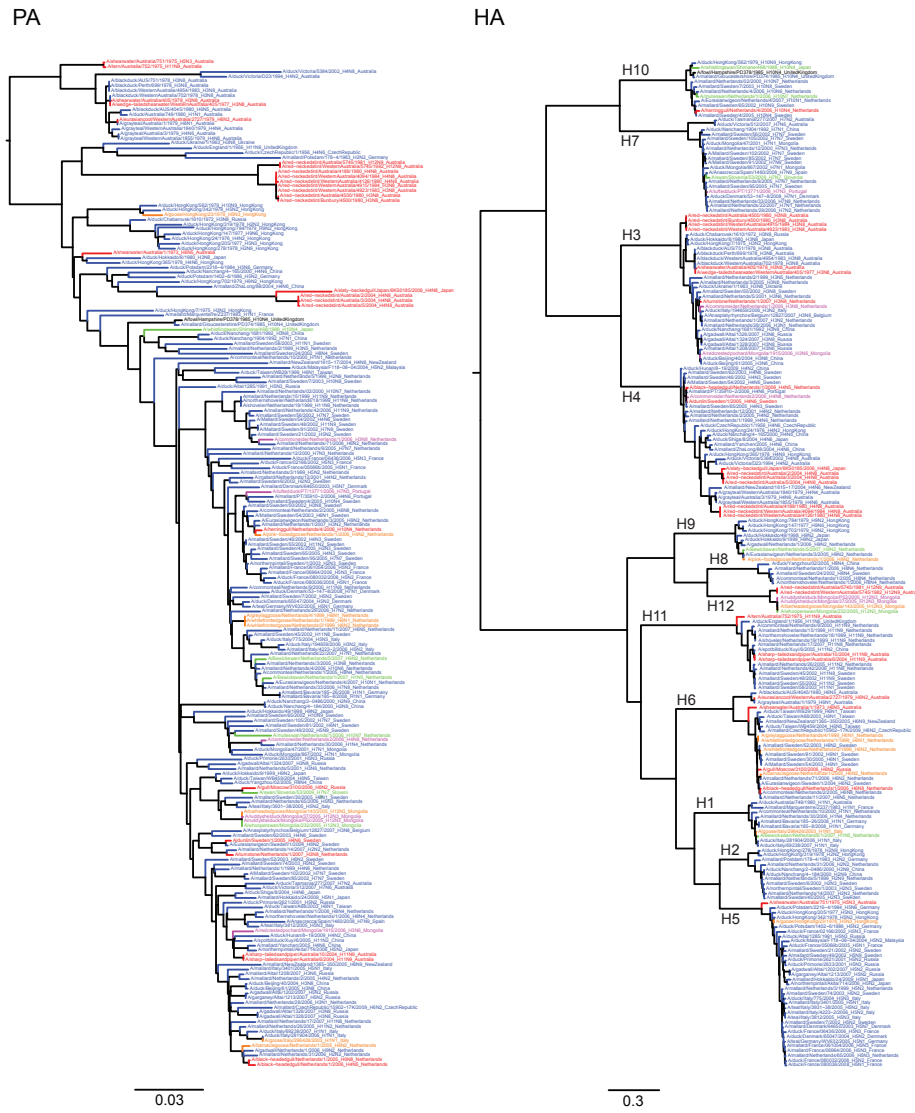


Figure S1c

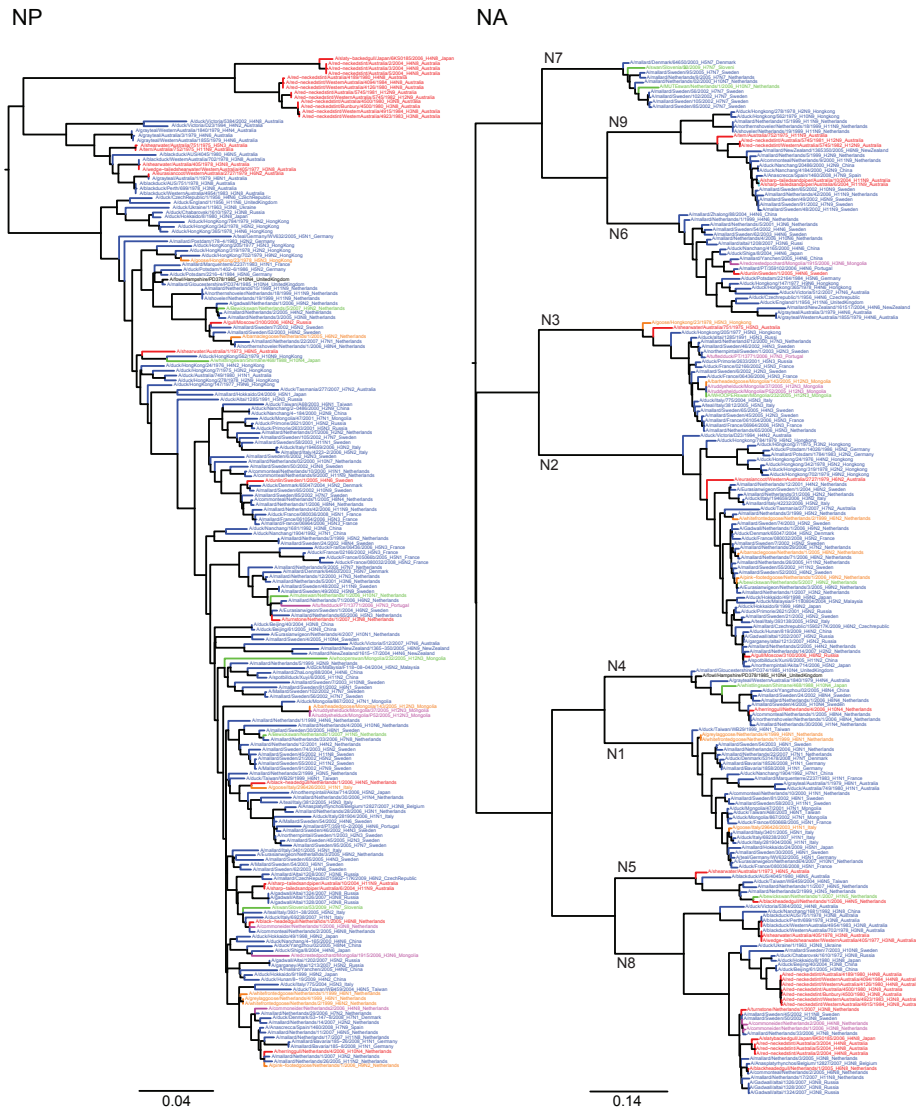


Figure S1d

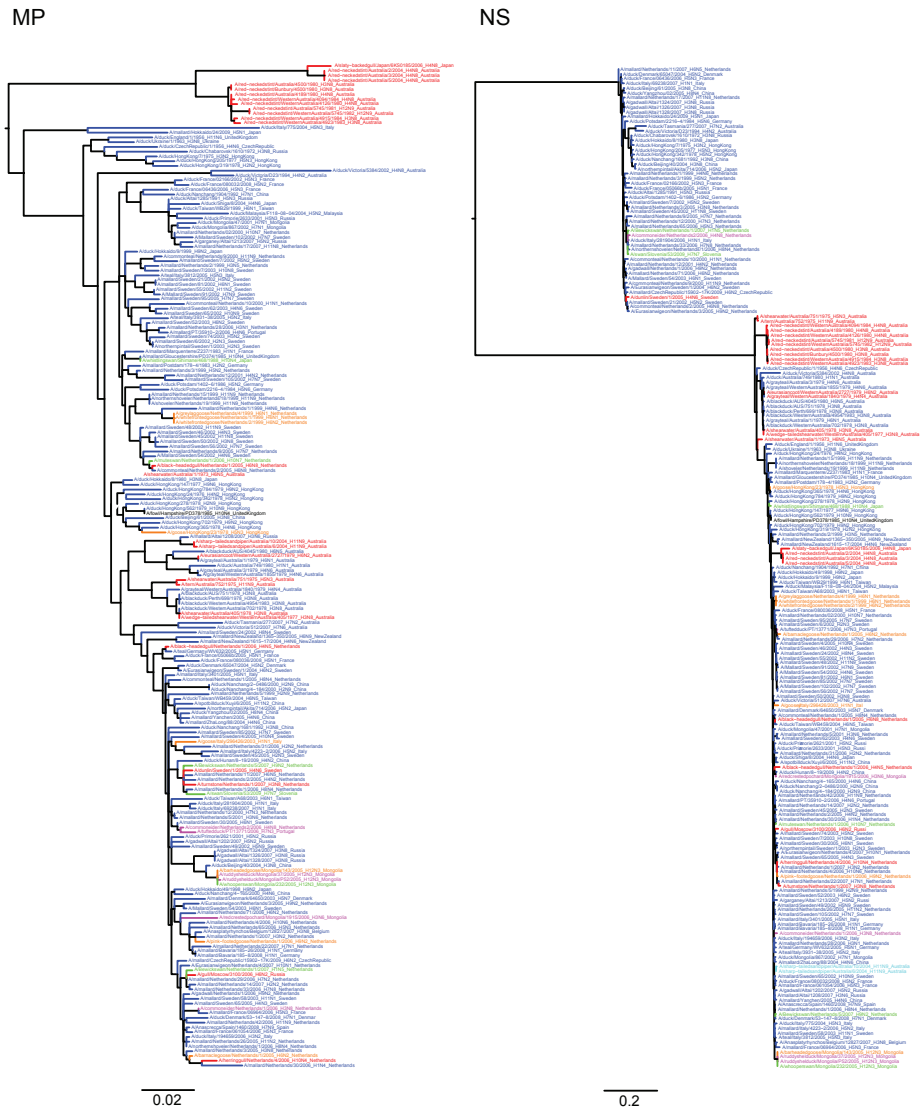
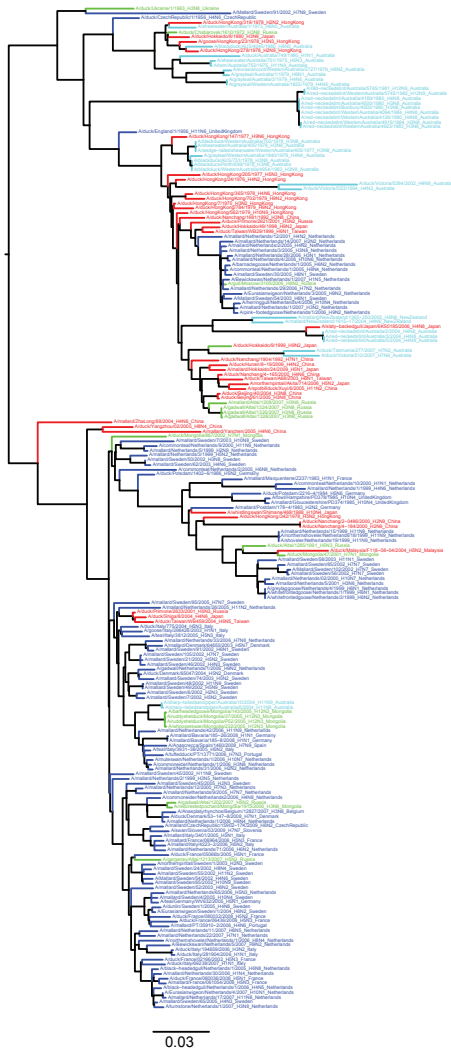


Figure S2a

PB2



PB1

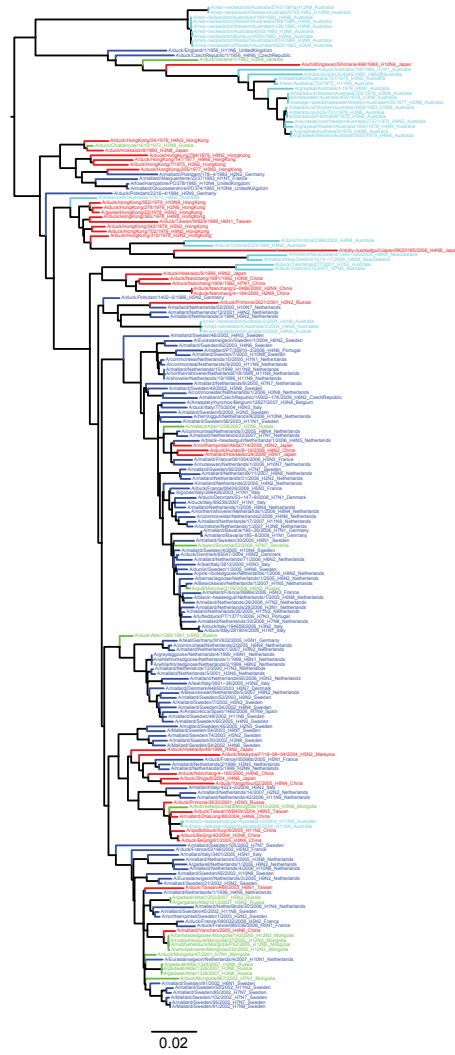


Figure S2b

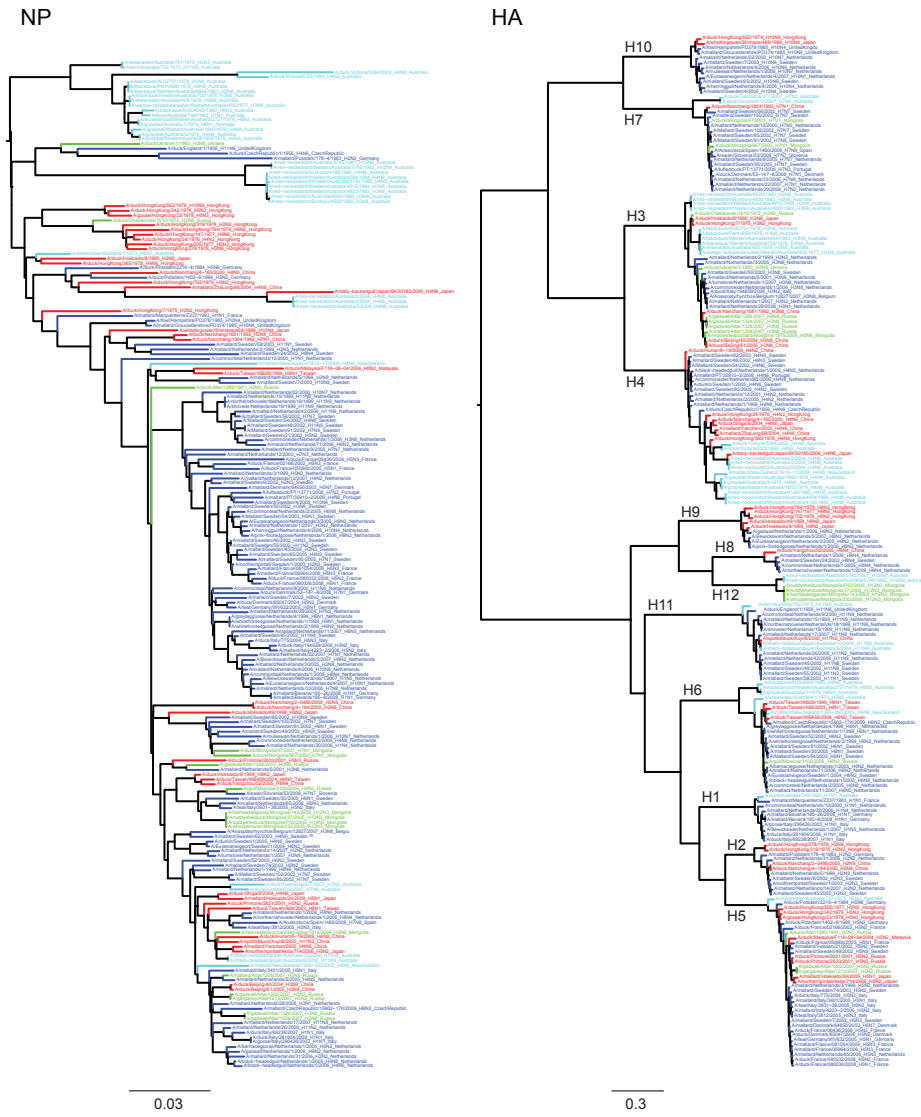


Figure S2c

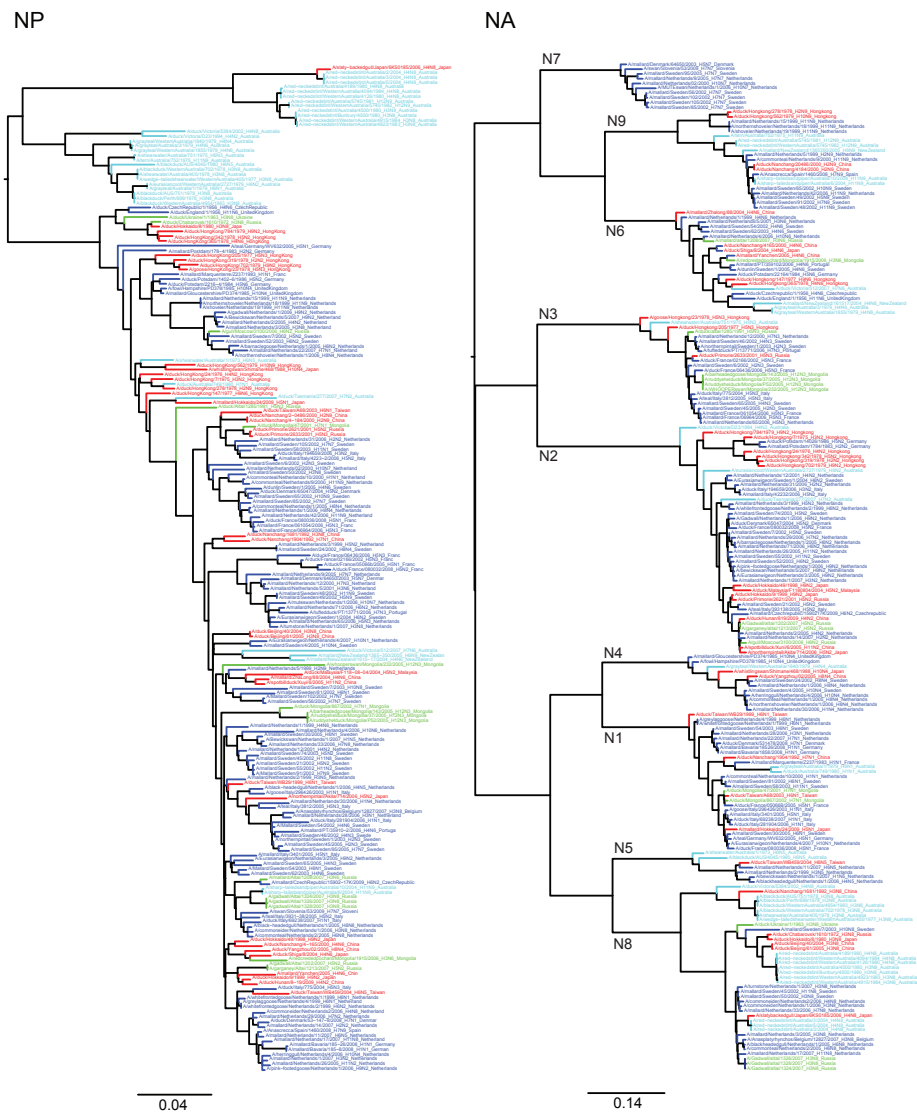


Figure S2d

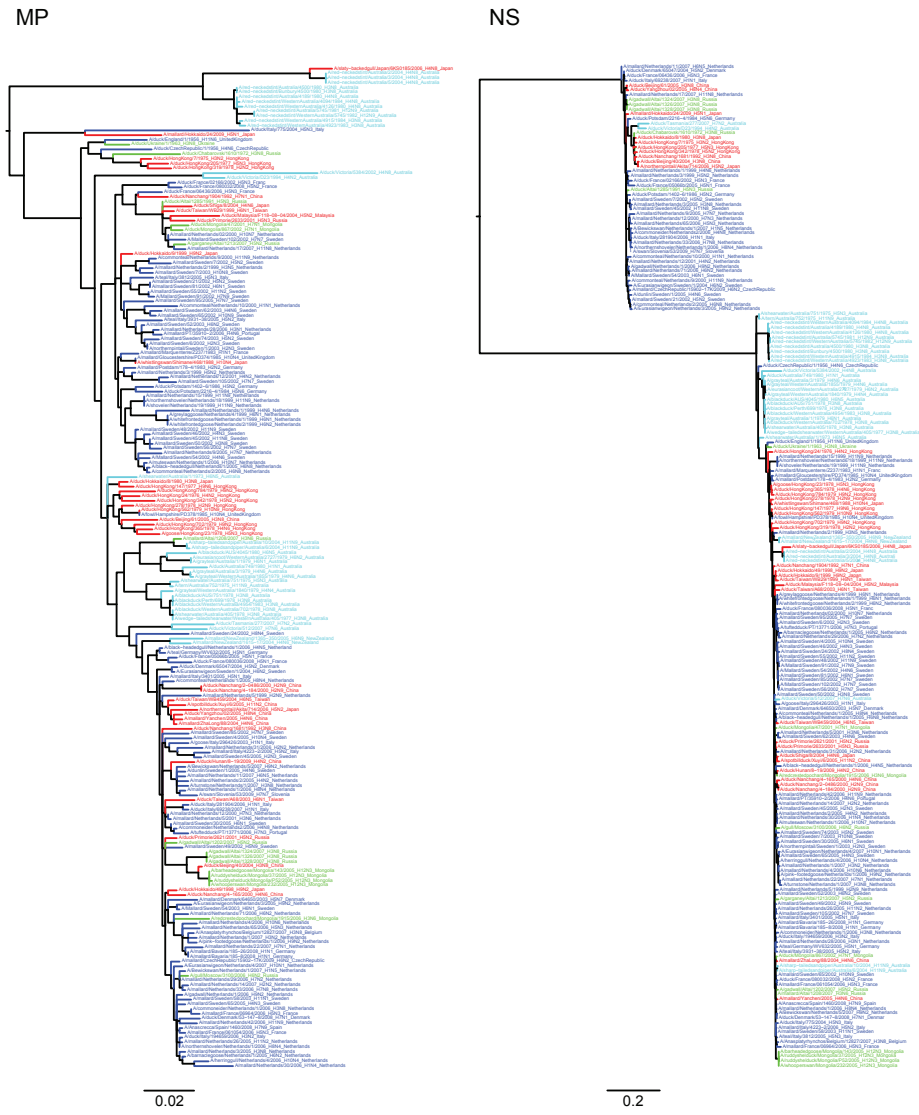


Figure S3a

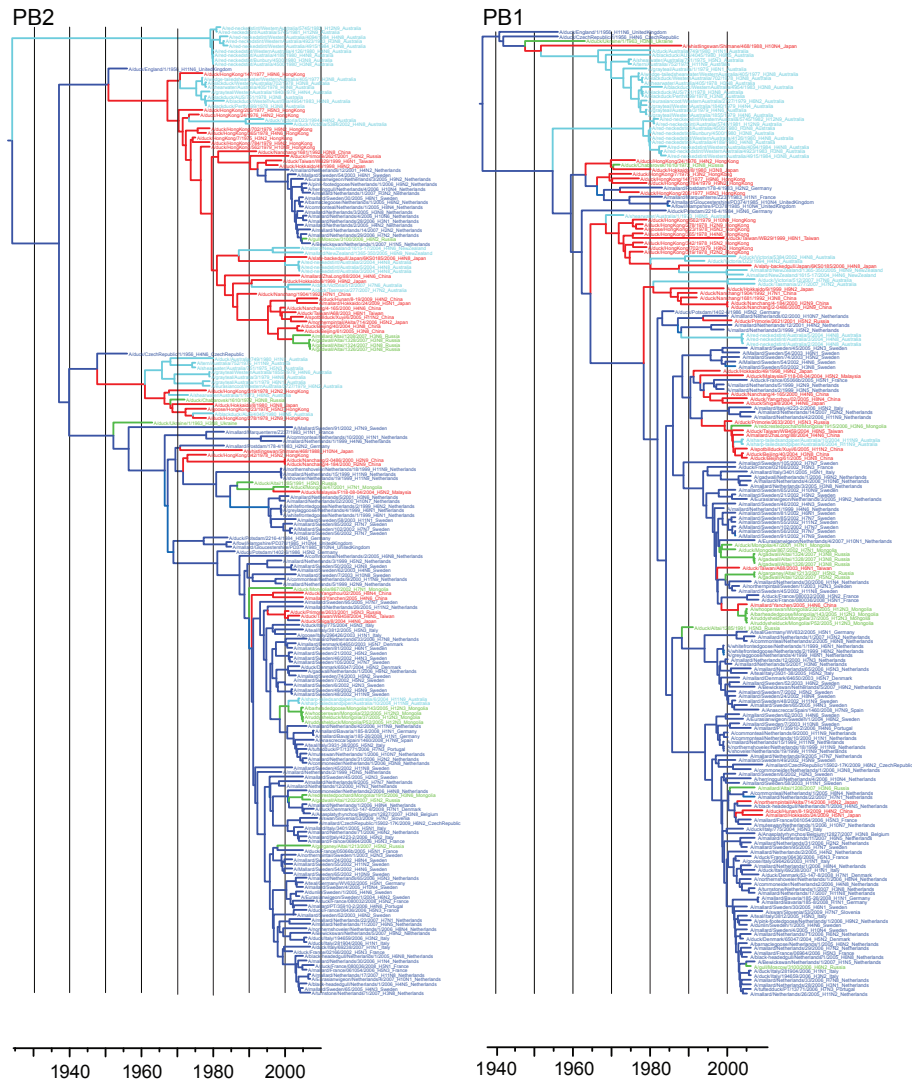


Figure S3b

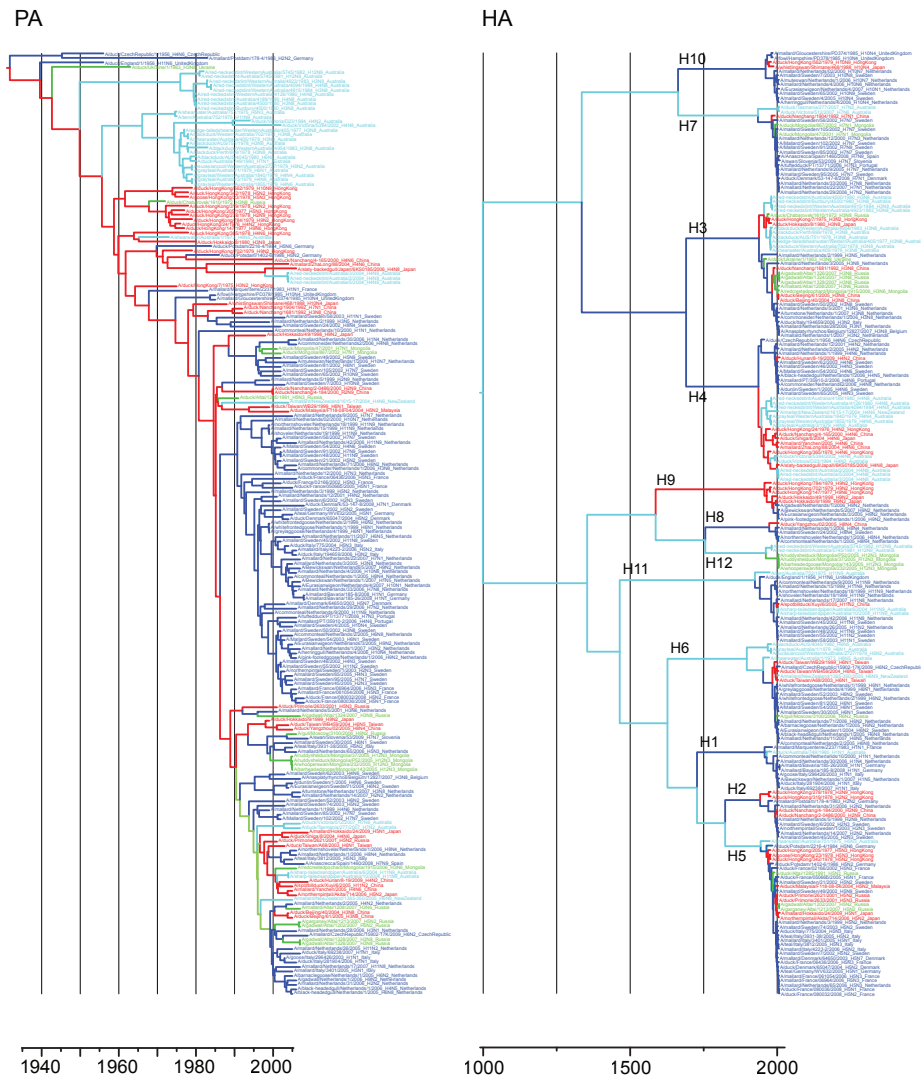


Figure S3c

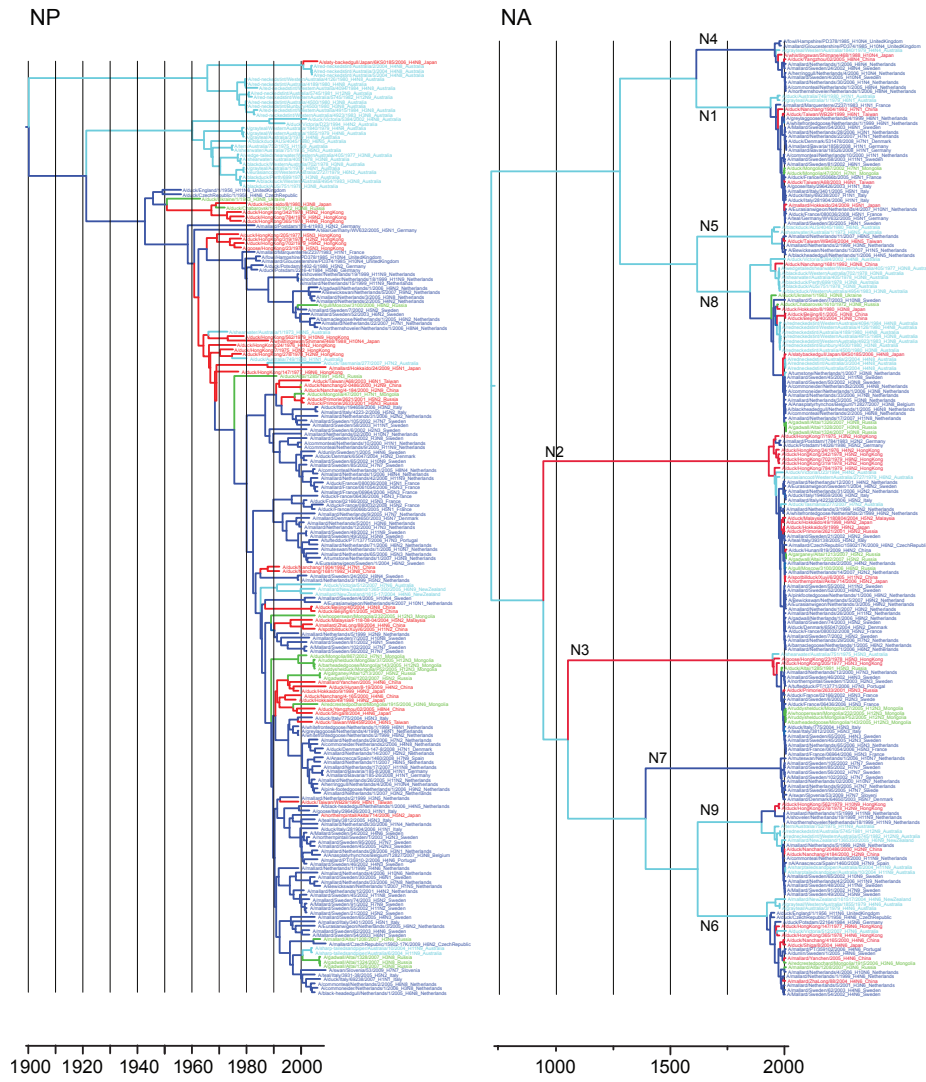


Figure S3d

